

# Check list for submitting Mass Chain Evaluations

- Run FMTCHK and correct all errors
- Run ConsistencyCheck and correct any issues
- Ensure that all relevant references from NSR have been included
- Ensure that Jpi values in the Adopted Levels are given with justification
- Ensure that  $T_{1/2}$  values in the Adopted Levels are traceable
- Ensure that Eg, Ig, Mult and MR in the Adopted Gammas are traceable
- Check that G.S. and isomer properties in Adopted Levels match exactly those corresponding properties in the parent records
- Ensure that all isomers are flagged with M (or M1,M2...) in column 78-79
- Check band drawings for incorrectly flagged levels or missing flags
- Ensure the  $J^{\pi}$ , Mult, and MR values in Decay Datasets are identical to those in the Adopted Levels
- Confirm that the latest version of BrIcc has been run on all datasets requiring ICC values
- Ensure the procedure for the normalization for decay datasets is clearly indicated
- Confirm that all decay datasets have been updated with latest Q values and log ft or HF codes run with updated Q values.
- Check that XUNDL datasets have not been exactly copied into evaluation (XUNDL datasets should be merged with existing datasets, not adopted as is)
- Check the reference titles for keynumbers that don't belong to the evaluation

